#7

1648

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/509,612

DATE: 03/12/2001
TIME: 10:39:58

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\03122001\I509612.raw

ENTERED

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TECH CENTER 1600/2900

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 4 <110> APPLICANT: ABRIGNANI, SERGIO
 5        GRANDI, GUIDO
 7 <120> TITLE OF INVENTION: HEPATITIS C RECEPTOR PROTEIN
 9 <130> FILE REFERENCE: PP00366.103
11 <140> CURRENT APPLICATION NUMBER: US 09/509,612
12 <141> CURRENT FILING DATE: 2000-03-29
14 <160> NUMBER OF SEQ ID NOS: 20
16 <170> SOFTWARE: Microsoft Word 97
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 49
20 <212> TYPE: DNA
21 <213> ORGANISM: Artificial Sequence
23 <220> FEATURE:
24 <223> OTHER INFORMATION: Description of Artificial
25        Sequence:oligodeoxynucleotides
27 <400> SEQUENCE: 1
28 ggcgggggtg gatccggggg tggaggctcg agctttgtca acaaggacc          49
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32 <212> TYPE: PRT
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35 <220> FEATURE:
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39 Phe Val Asn Lys Asp
40   1               5
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44 <211> LENGTH: 38
45 <212> TYPE: DNA
46 <213> ORGANISM: Artificial Sequence
48 <220> FEATURE:
49 <223> OTHER INFORMATION: Description of Artificial
50        Sequence:oligodeoxynucleotides
52 <400> SEQUENCE: 3
53 ccccaagctt tcacagcttc ccggagaaga ggtcatcg                     38
55 <210> SEQ ID NO: 4
56 <211> LENGTH: 8
57 <212> TYPE: PRT
58 <213> ORGANISM: Artificial Sequence
60 <220> FEATURE:
61 <223> OTHER INFORMATION: Description of Artificial Sequence:peptide
63 <400> SEQUENCE: 4
64 Leu Lys Gly Ser Phe Leu Asp Asp
65   1               5
68 <210> SEQ ID NO: 5
69 <211> LENGTH: 41
70 <212> TYPE: DNA
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71 <213> ORGANISM: Artificial Sequence
73 <220> FEATURE:
74 <223> OTHER INFORMATION: Description of Artificial
75   Sequence:oligodeoxynucleotides
77 <400> SEQUENCE: 5
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80 <210> SEQ ID NO: 6
81 <211> LENGTH: 9
82 <212> TYPE: PRT
83 <213> ORGANISM: Artificial Sequence
85 <220> FEATURE:
86 <223> OTHER INFORMATION: Description of Artificial Sequence:peptide
88 <400> SEQUENCE: 6
89 Phe Val Asn Lys Asp Gln Ile Ala Lys
90   1   5
93 <210> SEQ ID NO: 7
94 <211> LENGTH: 47
95 <212> TYPE: DNA
96 <213> ORGANISM: Artificial Sequence
98 <220> FEATURE:
99 <223> OTHER INFORMATION: Description of Artificial
100   Sequence:oligodeoxynucleotides
102 <400> SEQUENCE: 7
103 ccccaagctt tcaatgatga tgatgatgat gcagcttccc ggagaag   47
105 <210> SEQ ID NO: 8
106 <211> LENGTH: 11
107 <212> TYPE: PRT
108 <213> ORGANISM: Artificial Sequence
110 <220> FEATURE:
111 <223> OTHER INFORMATION: Description of Artificial Sequence:peptide
113 <400> SEQUENCE: 8
114 His His His His His His Leu Lys Gly Ser Phe
115   1   5   10
118 <210> SEQ ID NO: 9
119 <211> LENGTH: 20
120 <212> TYPE: DNA
121 <213> ORGANISM: Artificial Sequence
123 <220> FEATURE:
124 <223> OTHER INFORMATION: Description of Artificial
125   Sequence:oligodeoxynucleotides
127 <400> SEQUENCE: 9
128 cggttccgca gaccactatg   20
130 <210> SEQ ID NO: 10
131 <211> LENGTH: 21
132 <212> TYPE: DNA
133 <213> ORGANISM: Artificial Sequence
135 <220> FEATURE:
136 <223> OTHER INFORMATION: Description of Artificial
137   Sequence:oligodeoxynucleotides

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139 <400> SEQUENCE: 10                                      21
140 tcttcacgca gaaagcgtct a
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143 <211> LENGTH: 23
144 <212> TYPE: DNA
145 <213> ORGANISM: Artificial Sequence
147 <220> FEATURE:
148 <223> OTHER INFORMATION: Description of Artificial
149       Sequence:oligodeoxynucleotide
151 <400> SEQUENCE: 11                                      23
152 tgagtgtcgt gcagcctcca gga
154 <210> SEQ ID NO: 12
155 <211> LENGTH: 357
156 <212> TYPE: DNA
157 <213> ORGANISM: Artificial Sequence
159 <220> FEATURE:
160 <223> OTHER INFORMATION: Description of Artificial Sequence: Human EC2
161       fragment cloned into pThio-His C
163 <400> SEQUENCE: 12
164 gagttcctcg acgctaacct ggccggctct ggatccggtg atgacgatga caaggtacct 60
165 ggcatgctga gctcgagctt tgtcaacaag gaccagatcg ccaaggatgt gaagcagttc 120
166 tatgaccagg ccctacagca ggccgtggtg gatgatgacg ccaacaacgc caaggctgtg 180
167 gtgaagacct ccacgagac gcttgactgc tgtggctcca gcacactgac tgctttgacc 240
168 acctcagtgc tcaagaacaa tttgtgtccc tcgggcagca acatcatcag caacctcttc 300
169 aaggaggact gccaccagaa gatcgatgac ctcttctccg ggaagctgtg aaagctt    357
171 <210> SEQ ID NO: 13
172 <211> LENGTH: 116
173 <212> TYPE: PRT
174 <213> ORGANISM: Artificial Sequence
176 <220> FEATURE:
177 <223> OTHER INFORMATION: Description of Artificial Sequence:Deduced amino
178       acid sequence of EC2 fragment
180 <400> SEQUENCE: 13
181 Glu Phe Leu Asp Ala Asn Leu Ala Gly Ser Gly Ser Gly Asp Asp Asp
182  1               5                  10                  15
184 Asp Lys Val Pro Gly Met Leu Ser Ser Phe Val Asn Lys Asp Gln
185          20                  25                  30
187 Ile Ala Lys Asp Val Lys Gln Phe Tyr Asp Gln Ala Leu Gln Gln Ala
188          35                  40                  45
190 Val Val Asp Asp Asp Ala Asn Asn Ala Lys Ala Val Val Lys Thr Phe
191      50                  55                  60
193 His Glu Thr Leu Asp Cys Cys Gly Ser Ser Thr Leu Thr Ala Leu Thr
194  65                  70                  75                  80
196 Thr Ser Val Leu Lys Asn Asn Leu Cys Pro Ser Gly Ser Asn Ile Ile
197                  85                  90                  95
199 Ser Asn Leu Phe Lys Glu Asp Cys His Gln Lys Ile Asp Asp Leu Phe
200              100                 105                 110
202 Ser Gly Lys Leu
203          115
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206 <210> SEQ ID NO: 14
207 <211> LENGTH: 348
208 <212> TYPE: DNA
209 <213> ORGANISM: Artificial Sequence
211 <220> FEATURE:
212 <223> OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
213   sequence of EC20His6 fragment cloned into pGEX-KG
215 <400> SEQUENCE: 14
216 ctggttccgc gtggatcccc gggaatttcc ggtggtggtg gtggaattct atttgtcaac 60
217 aaggaccaga tcgccaagga tgtgaagcag ttctatgacc aggccctaca gcaggccgtg 120
218 gtggatgatg acgccaacaa cgccaaggct gtggtgaaga ccttccacga gacgcttgac 180
219 tgctgtggct ccagcacact gactgctttg accacctcag tgctcaagaa caatttgtgt 240
220 ccctcgggca gcaacatcat cagcaacctc ttcaaggagg actgccacca gaagatcgat 300
221 gacctcttct ccgggaagct gcatcatcat catcatcatt gaaagctt 348
223 <210> SEQ ID NO: 15
224 <211> LENGTH: 113
225 <212> TYPE: PRT
226 <213> ORGANISM: Artificial Sequence
228 <220> FEATURE:
229 <223> OTHER INFORMATION: Description of Artificial Sequence: Deduced amino
230   acid sequence of EC2-His 6 fragment
232 <400> SEQUENCE: 15
233 Leu Val Pro Arg Gly Ser Pro Gly Ile Ser Gly Gly Gly Gly Gly Ile
234 1   5   10   15
236 Leu Phe Val Asn Lys Asp Gln Ile Ala Lys Asp Val Lys Gln Phe Tyr
237   20   25   30
239 Asp Gln Ala Leu Gln Gln Ala Val Val Asp Asp Asp Ala Asn Asn Ala
240   35   40   45
242 Lys Ala Val Val Lys Thr Phe His Glu Thr Leu Asp Cys Cys Gly Ser
243   50   55   60
245 Ser Thr Leu Thr Ala Leu Thr Thr Ser Val Leu Lys Asn Asn Leu Cys
246 65   70   75   80
248 Pro Ser Gly Ser Asn Ile Ile Ser Asn Leu Phe Lys Glu Asp Cys His
249   85   90   95
251 Gln Lys Ile Asp Asp Leu Phe Ser Gly Lys Leu His His His His His
252   100   105   110
254 His
256 <210> SEQ ID NO: 16
257 <211> LENGTH: 236
258 <212> TYPE: PRT
259 <213> ORGANISM: Pan troglodytes
261 <400> SEQUENCE: 16
262 Met Gly Val Glu Gly Cys Thr Lys Cys Ile Lys Tyr Leu Leu Phe Val
263 1   5   10   15
265 Phe Asn Phe Val Phe Trp Leu Ala Gly Gly Val Ile Leu Gly Val Ala
266   20   25   30
268 Leu Trp Leu Arg His Asp Pro Gln Thr Thr Asn Leu Leu Tyr Leu Glu
269   35   40   45
271 Leu Gly Asp Lys Pro Ala Pro Asn Thr Phe Tyr Val Gly Ile Tyr Ile

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272      50                   55                   60
274 Leu Ile Ala Val Gly Ala Val Met Met Phe Val Gly Phe Leu Gly Cys
275 65                   70                   75                   80
277 Tyr Gly Ala Ile Gln Glu Ser Gln Cys Leu Leu Gly Thr Phe Phe Thr
278                   85                   90                   95
280 Cys Leu Val Ile Leu Phe Ala Cys Glu Val Ala Ala Gly Ile Trp Gly
281                  100                  105                  110
283 Phe Val Asn Lys Asp Gln Ile Ala Lys Asp Val Lys Gln Phe Tyr Asp
284             115                  120                  125
286 Gln Ala Leu Gln Gln Ala Val Val Asp Asp Asp Ala Asn Asn Ala Lys
287        130                  135                  140
289 Ala Val Val Lys Thr Phe His Glu Thr Leu Asp Cys Cys Gly Ser Ser
290 145                  150                  155                  160
292 Thr Leu Thr Ala Leu Thr Thr Ser Val Leu Lys Asn Asn Leu Cys Pro
293                  165                  170                  175
295 Ser Gly Ser Asn Ile Ile Ser Asn Leu Phe Lys Glu Asp Cys His Gln
296             180                  185                  190
298 Lys Ile Asp Asp Phe Phe Ser Gly Lys Leu Tyr Leu Ile Gly Ile Ala
299        195                  200                  205
301 Ala Ile Val Val Ala Val Ile Met Ile Phe Glu Met Ile Leu Ser Met
302     210                  215                  220
304 Val Leu Cys Cys Gly Ile Arg Asn Ser Ser Val Tyr
305 225                  230                  235
307 <210> SEQ ID NO: 17
308 <211> LENGTH: 236
309 <212> TYPE: PRT
310 <213> ORGANISM: Cercopithecus aethiops
312 <400> SEQUENCE: 17
313 Met Gly Val Glu Gly Cys Thr Lys Cys Ile Lys Tyr Leu Leu Phe Val
314 1               5                   10                   15
316 Phe Asn Phe Val Phe Trp Leu Ala Gly Gly Val Ile Leu Gly Val Ala
317                   20                   25                   30
319 Leu Trp Leu Arg His Asp Pro Gln Thr Thr Asn Leu Leu Tyr Leu Glu
320             35                   40                   45
322 Leu Gly Asp Lys Pro Ala Pro Asn Thr Ser Tyr Val Gly Ile Tyr Ile
323     50                   55                   60
325 Leu Ile Ala Val Gly Ala Val Met Met Phe Val Gly Phe Leu Gly Cys
326 65                   70                   75                   80
328 Tyr Gly Ala Ile Gln Glu Ser Gln Cys Leu Leu Gly Thr Phe Phe Thr
329                   85                   90                   95
331 Cys Leu Val Ile Leu Phe Ala Cys Glu Val Ala Ala Gly Ile Trp Gly
332                  100                  105                  110
334 Phe Val Asn Lys Asp Gln Ile Ala Lys Asp Val Lys Gln Phe Tyr Asp
335             115                  120                  125
337 Gln Ala Leu Gln Gln Ala Val Val Asp Asp Asp Ala Asn Asn Ala Lys
338        130                  135                  140
340 Ala Val Val Lys Thr Phe His Glu Thr Val Asp Cys Cys Gly Ser Ser
341 145                  150                  155                  160
343 Thr Leu Ala Ala Leu Thr Thr Ser Val Leu Lys Asn Asn Leu Cys Pro
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